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Prevalence and phylogenetic analysis of gastrointestinal helminths (Nematoda: Trichostrongylidae) in ruminant livestock of northwest Iran

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Abstract: Trichostrongylidae family is considered as a group of gastrointestinal nematodes of ruminants with widespread distribution in the world. The parasites are the major causes of productivity loss in many countries including Iran. This study was carried out to determine the distribution of abomasal Trichostrongylidae among livestock of Qazvin, Iran. Totally, 160 abomasum samples including 83 from sheep, 72 from cattle and 5 from goats were collected from slaughterhouses throughout the Qazvin Province. The ribosomal DNA internal transcribed spacer 2 (ITS2) region was amplified using PCR followed by sequencing 13 different isolates. Phylogenetic analysis of the identified sequences was performed using MEGA 7 software. The prevalence rate of the nematodes was 19.4% among the specimens. Also, two spices including *Marshallagia marshalli* and *Teladorsagia circumcincta* were identified among the isolates with *M. marshalli* at higher frequency. No *Trichostrongylus* spp. was detected in the region. Since livestock plays a major role in ecosystem balance and as some species of nematodes have a zoonotic nature, it is necessary to proceed with more comprehensive epidemiologic studies to clarify the infection rate among the human population living in the region.

Keywords: Iran, ITS2-rDNA region, Phylogenetic analysis, Qazvin, Trichostrongylidae.

Introduction

The family of Trichostrongylidae is considered as the most important gastrointestinal parasites among sylvatic and domesticated ruminants with worldwide distribution (19, 38). Several species of the family were reported such as *Teladorsagia circumcincta*, *Marshallagia marshalli* and *Trichostrongylus* spp. (19, 33, 34, 38).

Human infection by *Trichostrongylus* spp. could occur by ingesting the infective-stage larvae or through skin penetration by larvae (14). Human infections are frequently free of apparent clinical symptoms, although gastrointestinal signs may occur in some patients (31, 39). The importance of veterinary medicine is not seriously taken into account and this has caused reduced production, economic losses, and public health concerns. These nematodes are considered as major causes of veterinary and zoonotic infections (12, 32). Differentiation and improved diagnosis between the species are necessary for control programs as effective control strategies can lead to positive effect over the economy of different countries (3).

Conventional methods based on morphological characters such as spicules, gubernaculum, and caudal bursa in male worms are reliable to detect the species nevertheless, these methods cannot discern the species of female worms (12, 31).

Molecular biology assays are applied for identification and phylogenetic analysis of different species of nematodes (38). Although several ribosomal and mitochondrial regions were used to survey the nematodes, investigating the ribosomal DNA sequencing (particularly the ITS2 region) has been shown to be a useful tool for this purpose as the ITS-2 gene region can clarify the intraspecific homogeneity and interspecific divergence of sequence in the species of gastrointestinal nematodes (5, 20, 31, 36).

It is well documented that Iranian researchers have a long term experience over examining the gastrointestinal nematodes among humans and animals by morphological features (2, 7, 11). Domestically, recent molecular analysis studies are limited to few investigations concerning the diagnosis of *Trichostrongylus* species,